

AMENDMENTS TO THE CLAIMS

The following listing of claims will replace all prior versions and listing of claims in the application.

Listing of Claims

1. **(currently amended)** A method for use in a computer system for finding translation initiation codons in a nucleotide sequence, comprising:

a) analyzing a first data set to measure a combination of at least two of the features of initiator codons and pseudoinitiator codons provided in Table 1 to produce scoring function parameters for said combination of features;

b) reading a sequence in the vicinity of an ATG triplet and using one or more scoring functions and one or more of the scoring function parameters to determine a numerical score that quantifies how much said ATG triplet resembles an initiator codon;

c) generating a quadratic discriminant function by using Quadratic Discriminant Analysis with selecting a combination of feature variables that optimally classify ATG triplets in a nucleotide sequence as initiator codons or as pseudoinitiator codons based on the numerical score determined in step b) ~~to generate a quadratic discriminant function and Bayes Network construction; [[and]]~~

d) analyzing a second data set of nucleotide sequences using said quadratic discriminant function, wherein said analysis comprises evaluating at least one scoring function for each ATG triplet in said sequences to calculate the probability whether each ATG triplet is an initiator codon; [[and]]

e) locating translation initiation codons in said second data set based on the probability calculated in step d); and

f) transmitting the located translation initiation condons to a user of the computer system.

2. (canceled).

3. (original) A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said scoring functions from step d) comprise at least two of the scoring functions provided in Table 2.

4. (previously presented) A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said combination of feature variables from step c) comprises any combination of at least two of the feature variables provided in Table 3 wherein the combination comprises one feature variable from each of any two feature variable classes and results in a correlation coefficient for the feature variable combination greater than 0.9.

5. (previously presented) A method for finding translation initiation codons in a nucleotide sequence, as recited in claim 1, wherein said combination of feature variables from step c) comprises any combination of at least two of the feature variables provided in Table 3 wherein the combination comprises one feature variable from each of any two feature variable classes and results in a correlation coefficient for the feature variable combination greater than 0.8.